



# 4

# SEQUENCE LISTING

<110> Allen, Keith D.

<120> TRANSGENIC MICE CONTAINING PROTEIN  
PHOSPHATASE 2C GENE DISRUPTIONS

<130> R-775

<140> US 09/900,715

<141> 2001-07-06

<150> US 60/216,104

<151> 2000-07-06

<150> US 60/223,386

<151> 2000-08-07

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 996

<212> DNA

<213> Mus musculus

<400> 1

```
gagactgcag cagaatatgt aaaatctcga ctcccagagg ctcttaagca gcaccttcag 60
gattatgaga aggacaaaga aaacagtgtt ctgacctacc agaccatcct cgagcagcag 120
atcttgtcaa ttgaccggga aatgctggaa aagttgacag tctcctatga tgaagcaggc 180
acaacgtgtt tgatcscetct actctcagat aaagacctca ccgtggccaa cgttgggtgac 240
tctcggggag tcttgtgtga caaagatggc aatgccatcc ccttgtctca cgatcacaaag 300
ccttaccagc tgaaggaaag gaagaggata aagagagctg gtgggttcat cagctttaat 360
ggctcctgga ggggccaggg aatcctagcc atgtctcgat ccctgggaga ctatccactg 420
aaaaatctca acgtgggtcat cccagaccca gacatcttga cctttgacct ggacaagctg 480
cagccggagt tcatgatctt ggcctcagat ggcctgtggg atgctttcag caatgaagaa 540
gcgggttcgat tcatcaagga gcgcttggat gagccccact ttggggccaa aagcatcgtc 600
ctgcagtcct tttacagagg ctgccctgac aacatcactg tcatggtggt gaagttcagg 660
aatagtagca aaacagaaga gcactgaacc ctgccagatc tcagctgccc caaactagag 720
gactctcaac atactgttct cttcatgtag taaaagggtg ggggtataatt aggatcatgc 780
gtcccaacac agaaccctct tccctgatgg ccttgaatcc ctttggagta ctgagcagag 840
ggttgggtcc cttgctgaca ccgcagaggg tgctaagttt gtgtccccc agcccttcta 900
tcagtgtttg aaacacatac gtaggtagcc acagatccca catatgaggc aaaggaaagg 960
caggccatat gttttccttc ttaataatgt actttt 996
```

<210> 2

<211> 228

<212> PRT

<213> Mus musculus

<220>

<221> VARIANT

<222> 66

<223> Xaa = Any Amino Acid

<400> 2

Glu Thr Ala Ala Glu Tyr Val Lys Ser Arg Leu Pro Glu Ala Leu Lys  
1 5 10 15

Gln His Leu Gln Asp Tyr Glu Lys Asp Lys Glu Asn Ser Val Leu Thr  
 20 25 30  
 Tyr Gln Thr Ile Leu Glu Gln Gln Ile Leu Ser Ile Asp Arg Glu Met  
 35 40 45  
 Leu Glu Lys Leu Thr Val Ser Tyr Asp Glu Ala Gly Thr Thr Cys Leu  
 50 55 60  
 Ile Xaa Leu Leu Ser Asp Lys Asp Leu Thr Val Ala Asn Val Gly Asp  
 65 70 75 80  
 Ser Arg Gly Val Leu Cys Asp Lys Asp Gly Asn Ala Ile Pro Leu Ser  
 85 90 95  
 His Asp His Lys Pro Tyr Gln Leu Lys Glu Arg Lys Arg Ile Lys Arg  
 100 105 110  
 Ala Gly Gly Phe Ile Ser Phe Asn Gly Ser Trp Arg Val Gln Gly Ile  
 115 120 125  
 Leu Ala Met Ser Arg Ser Leu Gly Asp Tyr Pro Leu Lys Asn Leu Asn  
 130 135 140  
 Val Val Ile Pro Asp Pro Asp Ile Leu Thr Phe Asp Leu Asp Lys Leu  
 145 150 155 160  
 Gln Pro Glu Phe Met Ile Leu Ala Ser Asp Gly Leu Trp Asp Ala Phe  
 165 170 175  
 Ser Asn Glu Glu Ala Val Arg Phe Ile Lys Glu Arg Leu Asp Glu Pro  
 180 185 190  
 His Phe Gly Ala Lys Ser Ile Val Leu Gln Ser Phe Tyr Arg Gly Cys  
 195 200 205  
 Pro Asp Asn Ile Thr Val Met Val Val Lys Phe Arg Asn Ser Ser Lys  
 210 215 220  
 Thr Glu Glu His  
 225

<210> 3  
 <211> 200  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Targeting vector

<400> 3  
 gctggtggcc ttggcagtga cgaaggtgaa ggaggggtgc ttgtggctca gctctgttgc 60  
 agcagaccag cttgtggtac actcaccag accggaacaa gctaacaggc tccctctgtc 120  
 tttccaggtg gggtcatcag ctttaatggc tcttgagggt tccaggggaat cctagccatg 180  
 tctcgatccc tgggagacta 200

<210> 4  
 <211> 200  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Targeting vector

<400> 4  
 tcgtcctgca gtccttttac agaggctgcc ctgacaacat cactgtcatg gtgggtgaagt 60  
 tcaggaatag tagcaaaaca gaagggcact gaaccctgcc agatctcagc tgcccaaac 120  
 tagaggactc tcaacatact gttctcttca tgtagtaaaa ggtgtgggta taattaggat 180  
 catgcgtccc aacacagaac 200